GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 14:20:36 ; Search time 3120 Seconds
(without alignments)
16454.279 Million cell updates/sec

Title: US-09-815-923-3
Perfect score: 1764
Sequence: 1 atgccgccgtcggacgcgcc.....ctaccctatgcaacctgtga 1764

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	891.2	50.5	3195	3	AY071023	AY071023 Drosophil
2	889.6	50.4	1869	3	DMU04809	U04809 Drosophila
3	885.4	50.2	2461	3	DMU02296	U02296 Drosophila
4	589	33.4	2340	10	CPU84498	U84498 Cavia porce
5	579.4	32.8	2015	10	RNSLC6A4	Y11024 R.norvegicu
6	579.4	32.8	2278	6	I12034	I12034 Sequence 6
7	579.4	32.8	2415	6	I12035	I12035 Sequence 8
8	579.4	32.8	2415	10	RRSERTRAN	X63253 R.rattus mR
9	579.4	32.8	3190	10	RNNTT	X63995 R.norvegicu
10	578.2	32.8	2576	10	AF013604	AF013604 Mus muscu
11	563.8	32.0	2595	4	AF119122	AF119122 Bos tauru
12	562.8	31.9	2357	10	MMSEROT	X66119 M.musculus
13	562	31.9	2207	9	AF285761	AF285761 Macaca mu
14	555.4	31.5	2751	10	RATSTRP	M79450 Rat seroton
15	555.4	31.5	2756	6	I25791	I25791 Sequence 1
16	552.6	31.3	2099	9	HSSERT	X70697 H.sapiens m
17	552.4	31.3	2508	6	I12036	I12036 Sequence 10
18	552.4	31.3	2508	9	HUM5HTTCS	L05568 Human Na+/C
19	552.4	31.3	2889	6	AX003385	AX003385 Sequence
20	547	31.0	2407	4	AF246893	AF246893 Ovis arie
21	524	29.7	1894	9	AF286026	AF286026 Macaca mu
22	522.4	29.6	1983	9	HUMNORTR	M65105 Human norad
23	519.8	29.5	1890	5	AF318177	AF318177 Danio rer
24	511.2	29.0	3188	4	BTNORADR	X79015 B.taurus mR
25	509.6	28.9	2255	4	BTU09198	U09198 Bos taurus
26	507.8	28.8	2062	9	AF286445	AF286445 Macaca mu
27	507.8	28.8	2062	9	AF286447	AF286447 Macaca fa
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33	504.6	28.6	3919	6	AR009502	AR009502 Sequence
34	504.6	28.6	3919	9	S46955	S46955 dopamine tr
35	504.6	28.6	3946	6	AX336170	AX336170 Sequence
36	504.6	28.6	3946	9	HUMSLC6A3M	M95167 Homo sapien
37	503	28.5	2020	9	S44626	S44626 dopamine tr
38	500	28.3	1854	10	MMU76306	U76306 Mus musculu
39	498.4	28.3	1872	10	MMU439987	AJ439987 Mus muscu
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41	488.4	27.7	2014	10	AB021970	AB021970 Rattus no
42	488.4	27.7	2221	10	AB021971	AB021971 Rattus no
43	484.6	27.5	2391	4	BOVDOPATR	M80234 Cow dopamin
44	469.2	26.6	1985	10	RATDTRSP	M80233 Rat cocaine
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ALIGNMENTS

RESULT 1
AY071023
LOCUS AY071023 3195 bp mRNA linear INV 20-DEC-2001
DEFINITION Drosophila melanogaster RE10485 full length cDNA.
ACCESSION AY071023
VERSION AY071023.1 GI:17945171
KEYWORDS FLI_CDNA.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 3195)
AUTHORS Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
Champe,M., Chavez,C., Dorsett,V., Dresnek,D., Farfan,D., Frise,E.,

George,R., Gonzalez,M., Guarin,H., Kronmiller,B., Li,P., Liao,G., Miranda,A., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M. and Celniker,S.

TITLE Direct Submission

JOURNAL Submitted (18-DEC-2001) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA

COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to cdna@fruitfly.berkeley.edu.

FEATURES Location/Qualifiers

source 1. .3195
/organism="Drosophila melanogaster"
/strain="y; cn bw sp"
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gene 1. .3195
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BASE COUNT 729 a 892 c 871 g 703 t

ORIGIN

Query Match 50.5%; Score 891.2; DB 3; Length 3195;
Best Local Similarity 71.7%; Pred. No. 1.1e-195;
Matches 1185; Conservative 0; Mismatches 458; Indels 9; Gaps 1;

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Qy        82 GTGGTGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTC 141
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Db       644 ATTCTGGTGGTCTCCGTGACGGAGAGGACTCGCGAGACCTGGGGACAGAAGGCGGAGTTC 703

Qy       142 CTGCTGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATC 201
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Db       704 CTCCTGGCCGTGATTGGGTTCGCAGTGGATCTGGGCAATGTGTGGCGCTTCCCGTACATC 763

Qy       202 TGTTACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGC 261
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Db      1004 GCCTCGTTCACATCCA---------AGTTGCCGTGGACGTCGTGCGATAATCCCTGGAAC 1054

Qy       502 ACGCCGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCG 561
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RESULT 2
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LOCUS DMU04809 1869 bp mRNA linear INV 29-JUN-1994
DEFINITION Drosophila melanogaster Canton S serotonin transporter mRNA, complete cds.
ACCESSION U04809
VERSION U04809.1 GI:506639
KEYWORDS .
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1869)
AUTHORS Demchyshyn,L.L., Pristupa,Z.B., Sugamori,K.S., Barker,E.L., Blakely,R.D., Wolfgang,W.J., Forte,M.A. and Niznik,H.B.
TITLE Cloning, expression, and localization of a chloride-facilitated, cocaine-sensitive serotonin transporter from Drosophila melanogaster
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (11), 5158-5162 (1994)
MEDLINE 94255490
PUBMED 8197200
REFERENCE 2 (bases 1 to 1869)
AUTHORS Niznik,H.B.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1993) Hyman B. Niznik, Laboratory of Molecular Neurobiology, Clarke Institute of Psychiatry, 250 College St., Toronto, Ontario, M5T 1R8, Canada
FEATURES Location/Qualifiers
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BASE COUNT 349 a 539 c 556 g 425 t
ORIGIN

Query Match 50.4%; Score 889.6; DB 3; Length 1869;
Best Local Similarity 71.7%; Pred. No. 2.4e-195;
Matches 1184; Conservative 0; Mismatches 459; Indels 9; Gaps 1;

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Qy        562 AAGGAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATG 621
Db        661 AAGGAGTTCTTTGAGCGAAAGGTTTTGGAGAGCTACAAGGGCAACGGGCTGGACTTCATG 720

Qy        622 GGGCCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTC 681
Db        721 GGTCCGGTGAAGCCCACGCTGGCACTCTGCGTCTTCGGGGTCTTTGTCCTGGTCTACTTC 780

Qy        682 TCCTTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCG 741
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Qy        742 TACGTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGC 801
Db        841 TATGTGGTGCTAATCATCCTGCTGGTTAGAGGAGTTTCCCTGCCCGGCGCGGACGAGGGC 900

Qy        802 ATACGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGAC 861
Db        901 ATCAAGTACTACCTAACCCCGGAGTGGCACAAACTGAAGAACTCCAAGGTCTGGATCGAC 960
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Qy       1042 GTTCAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTG 1101
              || || || |    ||| ||  |||| ||||| || || || || ||||||||||||||
Db       1141 GTCCAAAAGACCTCCATTGACAAGGTGGGCCTGGAGGGTCCGGGGCTGGTGTTCATCGTT 1200

Qy       1102 TACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTC 1161
              ||||| |||||||| |||||  |||| |||||  |||||||||  ||||||||||||||
Db       1201 TACCCGGAGGCCATAGCCACGATGAGTGGCTCGGTGTTCTGGAGCATCATCTTCTTCCTG 1260

Qy       1162 ATGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCT 1221
              ||||| |||||||||||||| |||||  || |||||  ||  | |||||  | |  || ||
Db       1261 ATGCTGATTACCCTGGGACTGGACAGCACCTTTGGCGGATTGGAGGCGATGATAACAGCG 1320

Qy       1222 CTTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTG 1281
              || |||||||| ||||| |||||| | |||||  |   | ||  | || ||     | ||
Db       1321 CTGTGCGACGAGTATCCGCGAGTGATTGGCAGGCGCAGGGAGCTGTTCGTCCTGCTGCTC 1380

Qy       1282 CTTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTA 1341
              ||    |||||||   | ||||| || |||||  |  || |||||||| ||    || ||
Db       1381 CTGGCCTTCATCTTCCTGTGCGCCCTTCCCACGATGACCTACGGTGGCGTGGTGCTGGTC 1440

Qy       1342 GACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCT 1401
              || | || ||||| || || || || ||||| || || || ||||| || |  |||||
Db       1441 AACTTCCTGAATGTCTACGGACCCGGGTTGGCCATCCTCTTTGTGGTCTTCGTGGAGGCA 1500

Qy       1402 GCCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTG 1461
              ||||| || |  ||| | || || || ||||| |||       ||||||       ||||||
Db       1501 GCCGGAGTCTTTTGGTTCTACGGAGTGGACCGCTTCAGCTCGGATGTGGAACAGATGCTG 1560

Qy       1462 GGGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTG 1521
              ||   ||  || || |  |||||| ||| ||| ||| | |||||||| || || ||| ||
Db       1561 GGCAGCAAGCCAGGCTTATTCTGGCGGATCTGCTGGACGTACATCAGCCCTGTGTTCCTG 1620

Qy       1522 CTGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACC 1581
              |||    | ||| | |||||| |  |||   || ||||||||||||||| ||| |||  |
Db       1621 CTGACCATATTCATTTTCTCCATCATGGGCTACAAGGAGATGCTCGGCGAGGAGTACTAC 1680

         1582 TATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATT 1641
              || ||    |||     |   || ||||||| | | ||| || |  | ||    |||||
Db       1681 TACCCGGACTGGAGCTACCAGGTGGGCTGGGCGGTCACCTGCTCGTCGGTGCTCTGCATC 1740

Qy       1642 CCTCTTTACATTATCTACAAACTGCTCATCAC 1673
              ||  | ||||||||||||||  |  || || |
Db       1741 CCCATGTACATTATCTACAAGTTCTTCTTCGC 1772
```

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RESULT 3
DMU02296
LOCUS       DMU02296               2461 bp    mRNA    linear   INV 29-JAN-1999
DEFINITION  Drosophila melanogaster cocaine-sensitive serotonin transporter
            mRNA, complete cds.
ACCESSION   U02296
VERSION     U02296.1  GI:406054
KEYWORDS    .
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 2461)
  AUTHORS   Corey,J.L., Quick,M.W., Davidson,N., Lester,H.A. and Guastella,J.
  TITLE     A cocaine-sensitive Drosophila serotonin transporter: cloning,
            expression, and electrophysiological characterization
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91 (3), 1188-1192 (1994)
  MEDLINE   94134723
   PUBMED   8302852
REFERENCE   2  (bases 1 to 2461)
  AUTHORS   Corey,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-1993) Corey J.L., California Institute of
            Technology, Biology, Pasadena, CA 91125, USA
FEATURES             Location/Qualifiers
     source          1. .2461
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="dSERT1"
                     /clone_lib="D. melanogaster head library"
                     /dev_stage="adult"
     CDS             109. .1854
                     /codon_start=1
                     /product="cocaine-sensitive serotonin transporter"
                     /protein_id="AAD10615.1"
                     /db_xref="GI:406055"
                     /translation="MATTRRRQGHRSTGPQAGQQRAHSGGFRDERTRETWGQKAEFLL
                     AVIGFAVDLGNVWRFPYICYQNGGGAFLVPYCLFLIFGGLPLFYMELALGQFHRCGCL
                     SIWKRICPALKGVGYAICLIDIYMGMYYNTIIGWAVYYLFASFTSKLPWTSCDNPWNT
                     ENCMQVTSENFTELATSPAKEFFERKVLESYKGNGLDFMGPVKPTLALCVFGVFVLVY
                     FSLWKGVRSAGKVVWVTALAPYVVLIILLVRGVSLPGADEGIKYYLTPEWHKLKNSKV
                     WIDAASQIFFSLGPGFGTLLALSSYNKFNNNCYRDALITSSINCLTSFLAGFVIFSVL
                     GYMAYVQKTSIDKVGLEGPGLVFIVYPEAIATMSGSVFWSIIFFLMLITLGLDSTFGG
                     LEAMITALCDEYPRVIGRRRELFVLLLLAFIFLCALPTMTYGGVVLVNFLNVYGPGLA
                     ILFVVFVEAAGVFWFYGVDRFSSDVEQMLGSKPGLFWRICWTYISPVFLLTIFIFSIM
                     GYKEMLGEEYYYPDWSYQVGWAVTCSSVLCIPMYIIYKFFFASKGGCRQRLQESFQPE
                     DNCGSVVPGQQGTSV"
BASE COUNT      508 a    719 c    687 g    547 t
ORIGIN
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  Query Match           50.2%;  Score 885.4;  DB 3;  Length 2461;
  Best Local Similarity 73.3%;  Pred. No. 2.3e-194;
  Matches 1151;  Conservative    0;  Mismatches  411;  Indels    9;  Gaps    1;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162
              | | ||   |||||||||||||   ||||||| |||||||| |||||  ||| | || |||
Db        196 GAGAGGACTCGCGAGACCTGGGGACAGAAGGCGGAGTTCCTCCTGGCCGTGATTGGGTTC 255

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222
              |||||||||||  || || |||||||| ||||| |||||||| || ||||| ||||||||
Db        256 GCAGTGGATCTGGGCAATGTGTGGCGCTTCCCGTACATCTGCTATCAGAACGGAGGCGGC 315

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282
              || |||||| | || |||||| |  | ||  | || || || ||||| ||||||| | ||
Db        316 GCCTTCCTGGTGCCCTACTGCCTCTTCCTCATCTTCGGTGGACTGCCCCTGTTCTACATG 375

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342
              || |||||||||||||||| |||||| || || |||||||   ||||||| || |||||
Db        376 GAGCTGGCGCTGGGCCAGTTCCACCGATGTGGTTGCCTCAGCATCTGGAAGCGCATCTGT 435

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402
              || || || ||||| || |||||||| |||||| | |||||||| || ||||||||||||
Db        436 CCGGCCCTAAAAGGCGTGGGCTATGCGATCTGCCTAATCGACATTTATATGGGCATGTAC 495

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAAC 462
              |||||||||| ||||| |||||||| || |||||  |||| ||  || | || |
Db        496 TACAACACGATTATCGGCTGGGCGGTATACTACCTCTTCGCCTCGTTCACATCCA----- 550

Qy        463 TCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTC 522
                  | |||| |||||    ||||| ||    ||||||||    |   |||| || |||
Db        551 ----AGTTGCCGTGGACGTCGTGCGATAATCCCTGGAACACTGAGAACTGCATGCAGGTG 606

Qy        523 ACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAAT 582
              |||       |   |          |  |  | ||||| |||||||||| || || ||
Db        607 ACCAGTGAGAACTTCACGGAACTGGCCACGTCGCCGGCCAAGGAGTTCTTTGAGCGAAAG 666

Qy        583 GTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTG 642
              || ||||||    |||||  ||||| ||||  |||||| ||| | |||||  |||||
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Db        667 GTTTTGGAGAGCTACAAGGGCAACGGGCTGGACTTCATGGGTCCGGTGAAGCCCACGCTG 726

Qy        643 GCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGG 702
              || || || || |||||||||||||||||| |||||||||||| ||||||| |||||  |
Db        727 GCACTCTGCGTCTTCGGGGTCTTTGTCCTGGTCTACTTCTCCCTGTGGAAGGGAGTGCGC 786

Qy        703 AGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTG 762
              ||||| || |||||||||||||| || |||||||| || || ||||||||  | || |||
Db        787 AGTGCCGGAAAGGTGGTGTGGGTCACCGCTCTGGCTCCTTATGTGGTGCTAATCATCCTG 846

Qy        763 CTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCA 822
              ||||  ||||| ||  | || || || |||   ||||||||    |||||||| |||||
Db        847 CTGGTTAGAGGAGTTTCCCTGCCCGGCGCGGACGAGGGCATCAAGTACTACCTAACCCCG 906

Qy        823 GAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTC 882
              |||||||||||| || | ||||| ||||| ||||| ||||| ||||||||||||||||||
Db        907 GAGTGGCACAAACTGAAGAACTCCAAGGTCTGGATCGACGCCGCATCCCAGATTTTCTTC 966

Qy        883 TCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAAC 942
              || || || ||||| |||||||||||| ||||| || ||||||||||||||||||||||||
Db        967 TCCCTGGGCCCCGGATTCGGAACCCTGCTGGCCCTGTCCAGCTACAACAAGTTCAACAAC 1026

Qy        943 AACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCT 1002
              ||||||||  | || || |||||||||       |||||||||||||||| || || ||
Db       1027 AACTGCTATCGCGATGCTCTCATCACCAGCAGCATCAACTGCTTGACCAGTTTTCTGGCC 1086

Qy       1003 GGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAG 1062
              || || ||||| ||||| |||||||||||||||||  |||| || || |    ||| ||
Db       1087 GGCTTTGTCATCTTCTCCGTTTTGGGGTACATGGCCTACGTCCAAAAGACCTCCATTGAC 1146

Qy       1063 GAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACC 1122
               |||| ||||| || || || || |||||||||||||| ||||| ||||||||| |||||
Db       1147 AAGGTGGGCCTGGAGGGTCCGGGGCTGGTGTTCATCGTTTACCCGGAGGCCATAGCCACG 1206

Qy       1123 ATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTT 1182
              ||||  ||||| |||||||||  |||||||||||||| ||||| |||||||||||||
Db       1207 ATGAGTGGCTCGGTGTTCTGGAGCATCATCTTCTTCCTGATGCTGATTACCCTGGGACTG 1266

Qy       1183 GACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGA 1242
              ||||| || ||||| ||  | ||||  | |  || || || |||||||| ||||| |||
Db       1267 GACAGCACCTTTGGCGGATTGGAGGCGATGATAACAGCGCTGTGCGACGAGTATCCGCGA 1326

Qy       1243 GTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGC 1302
              ||| | ||||| |  | || | || ||      | || ||    |||||||   | |||
Db       1327 GTGATTGGCAGGCGCAGGGAGCTGTTCGTCCTGCTGCTCCTGGCCTTCATCTTCCTGTGC 1386

Qy       1303 GCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGC 1362
              || || ||||| |  || |||||||| ||    || ||  || | || ||||| || ||
Db       1387 GCCCTTCCCACGATGACCTACGGTGGCGTGGTGCTGGTCAACTTCCTGAATGTCTACGGA 1446

Qy       1363 CCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTAT 1422
              || || ||||| || || || ||||| || |  ||||| ||||| || |  ||| | ||
Db       1447 CCCGGGTTGGCCATCCTCTTTGTGGTCTTCGTGGAGGCAGCCGGAGTCTTTTGGTTCTAC 1506

Qy       1423 GGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTC 1482
              || || ||||| |||      ||||||      ||||||||   ||  || || |  |||
Db       1507 GGAGTGGACCGCTTCAGCTCGGATGTGGAACAGATGCTGGGCAGCAAGCCAGGCTTATTC 1566

Qy       1483 TGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCC 1542
              ||| ||| ||| ||| | |||||||| || || ||| |||||     | ||| | ||||||
Db       1567 TGGCGGATCTGCTGGACGTACATCAGCCCTGTGTTCCTGCTGACCATATTCATTTTCTCC 1626

Qy       1543 GTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACC 1602
               |  |||   || |||||||||||||| ||| |||  ||| ||   |||     |
Db       1627 ATCATGGGCTACAAGGAGATGCTCGGCGAGGAGTACTACTACCCGGACTGGAGCTACCAG 1686

Qy       1603 GTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAA 1662
              || ||||||| | | ||| || |  | ||    ||||| ||  | ||||||||||||||
Db       1687 GTGGGCTGGGCGGTCACCTGCTCGTCGGTGCTCTGCATCCCCATGTACATTATCTACAAG 1746

Qy       1663 CTGCTCATCAC 1673
               |  || || |
Db       1747 TTCTTCTTCGC 1757
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RESULT 4
CPU84498
LOCUS       CPU84498                2340 bp    mRNA    linear   ROD 04-NOV-1997
DEFINITION  Cavia porcellus transmembrane 5-HT transporter mRNA, complete cds.
ACCESSION   U84498
VERSION     U84498.1  GI:2584854
KEYWORDS    .
SOURCE      Cavia porcellus.
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1  (bases 1 to 2340)
  AUTHORS   Wade,P.R., Chen,J., Jaffe,B., Kassem,I.S., Blakely,R.D. and
            Gershon,M.D.
  TITLE     Localization and function of a 5-HT transporter in crypt epithelia
            of the gastrointestinal tract
  JOURNAL   J. Neurosci. 16 (7), 2352-2364 (1996)
  MEDLINE   96180949
   PUBMED   8601815
REFERENCE   2  (bases 1 to 2340)
  AUTHORS   Chen,J., Wade,P.R., Rothman,T.P. and Gershon,M.D.
  TITLE     Guinea pig intestinal mucosal transmembrane 5-HT transporter
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 2340)
  AUTHORS   Chen,J., Wade,P.R., Rothman,T.P. and Gershon,M.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-1997) Anatomy & Cell Biology, Columbia University
            P&S, 630 W. 168th St., New York, NY 10032, USA
FEATURES             Location/Qualifiers
     source          1. .2340
                     /organism="Cavia porcellus"
                     /db_xref="taxon:10141"
                     /tissue_type="intestinal mucosa"
     CDS             16. .1908
                     /note="plasmalemmal serotonin transporter"
                     /codon_start=1
                     /product="transmembrane 5-HT transporter"
                     /protein_id="AAB82737.1"
                     /db_xref="GI:2584855"
                     /translation="METTALNSQKAPSVCKDREDCQENSILQKSGPTSAGGVESGQIF
                     NGYSSVPSTGMGDDAEHSVPTATTTLVAEVHHGERETWGKKVDFLLSVIGYAVDLGNI
                     WRFPYVCYQNGGGAFLLPYIIMAIFGGIPLFYMELALGQYHRNGCISIWRKICPIFKG
                     IGYTICIIAFYIASYYNTIIAWALYYLISSFTDRLPWTSCRNSWNTANCTNYFSEDNI
                     TWTLHSTSPAEEFYIRHILQIHRSKGLQDVGGVSWQLTLCIMLIFTIIYFSIWKGVKT
                     SGKVVWVTATFPYIVLSVLLVRGATLPGAWKGVLFYLKPNWQKLLETGVWIDAAAQIF
                     FSLGPGFGVLLAFASYNKFNNNCYQDALVTSAVNCMTSFVSGFVIFTVLGYMAEMRSE
                     DVSEVAKDAGPSLLFITYAEAIANMPASTFFAIIFFLMLITLGLDSTFAGLEGVITAV
                     LDEFPHIWAKHREWFVLAVVITCFFGSLTTLTFGGAYVVKLLEEYATGPAVLTVVFIE
                     AIAVSWFYGVTQFCSDVKEMLGFSPGWFWRICWVAVSPVFLLFIICSFLMSPPQLRLF
                     QYSYPHWSVILGYCIGTSSVICIPTYITYRLVTTPGTLKERIIKSITPETPTEIPCGD
                     ICLNAV"
BASE COUNT      533 a    599 c    589 g    619 t
ORIGIN

  Query Match             33.4%;  Score 589;  DB 10;  Length 2340;
  Best Local Similarity   60.4%;  Pred. No. 1e-125;
  Matches  989;  Conservative    0;  Mismatches  645;  Indels    3;  Gaps    1;

Qy         86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
              |||||  |      ||      || |||| ||||||||||  |||||||  ||| ||||| |
Db        224 TGGTGGCTGAGGTGCACCATGGGGAGCGGGAGACCTGGGGCAAGAAGGTAGACTTCCTCC 283

Qy        146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
              |  ||||  | || | ||| ||||| || || ||| | ||||| || |||||  | ||||
Db        284 TCTCGGTCATCGGCTACGCTGTGGACCTGGGCAACATCTGGCGCTTTCCCTATGTGTGTT 343

Qy        206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
              ||||||| || || || || ||||| |||| |||  | | |||    | ||||| |||
Db        344 ACCAGAACGGTGGAGGAGCATTCCTCCTCCCCTACATCATCATGGCCATCTTTGGAGGGA 403

Qy        266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
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Db        404 TCCCACTGTTTTACATGGAGCTTGCGTTGGGCCAGTATCACCGGAATGGATGCATTTCTA 463

Qy        326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385

Db        464 TATGGAGGAAAATCTGCCCGATTTTTAAAGGGATTGGCTACACCATCTGCATCATCGCCT 523

Qy        386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445

Db        524 TCTACATTGCCTCCTACTACAACACCATCATAGCCTGGGCCCTCTACTACCTCATCTCTT 583

Qy        446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505

Db        584 CCTTTACGGACCGGCTGCCCTGGACCAGTTGCAGGAACTCCTGGAACACGGCCAACTGCA 643

Qy        506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565

Db        644 CCAACTACTTCTCTGAGGACAACATCACCTGGACGCTCCACTCCACCTCCCCTGCGGAAG 703

Qy        566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625

Db        704 AGTTTTATATACGCCACATCCTTCAGATCCATCGGTCTAAGGGACTGCAGGACGTGGGAG 763

Qy        626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685

Db        764 GCGTCAGTTGGCAGCTTACTCTCTGCATCATGCTTATCTTTACCATCATATACTTCAGCA 823

Qy        686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745

Db        824 TCTGGAAAGGTGTTAAAACATCTGGCAAGGTGGTGTGGGTGACAGCTACCTTTCCTTATA 883

Qy        746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805

Db        884 TCGTCCTTTCTGTGCTGCTGGTGAGGGGGGCCACACTCCCAGGAGCGTGGAAGGGTGTTC 943

Qy        806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865

Db        944 TCTTCTACTTGAAACCCAACTGGCAGAAGCTCCTGGAGACAGGGGTGTGGATTGATGCTG 1003

Qy        866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925

Db       1004 CTGCTCAGATATTCTTCTCTCTTGGTCCAGGCTTTGGGGTCCTCCTGGCCTTTGCCAGCT 1063

Qy        926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985

Db       1064 ATAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGCGGTGAATTGCA 1123

Qy        986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045

Db       1124 TGACGAGCTTCGTTTCGGGGTTTGTGATCTTCACGGTACTGGGGTACATGGCTGAGATGA 1183

Qy       1046 AGAACAAGAGCATCGAGGAGGTTGGCCTCGA---AGGCCCTGGACTGGTGTTCATCGTGT 1102

Db       1184 GGAGCGAAGATGTATCTGAAGTAGCCAAAGATGCAGGCCCCAGCCTCCTCTTCATCACCT 1243

Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162

Db       1244 ATGCAGAGGCCATAGCCAACATGCCGGCATCCACGTTTTTTGCCATCATCTTCTTCCTCA 1303

Qy       1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222

Db       1304 TGTTAATCACACTGGGTCTGGACAGCACGTTTGCAGGCTTGGAGGGAGTGATCACTGCAG 1363

Qy       1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282

Db       1364 TGCTGGATGAGTTTCCACACATCTGGGCCAAGCACCGGGAGTGGTTTGTGCTTGCTGTGG 1423

Qy       1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342

Db       1424 TCATTACTTGCTTCTTTGGATCCCTGACCACCCTGACTTTTGGAGGGGCCTACGTGGTGA 1483

Qy       1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402

Db       1484 AGTTGCTGGAGGAGTACGCCACGGGGCCTGCGGTGCTCACCGTGGTGTTCATAGAAGCAA 1543

Qy       1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462

Db       1544 TCGCTGTGTCTTGGTTCTATGGGGTCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTCG 1603

Qy       1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522

Db       1604 GCTTCAGCCCGGGATGGTTTTGGAGGATCTGCTGGGTGGCGGTCAGCCCTGTGTTCCTCC 1663

Qy       1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582

Db       1664 TGTTCATCATCTGCAGTTTTCTGATGAGCCCACCCCAGCTACGACTTTTCCAATACAGTT 1723

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642

Db       1724 ATCCCCACTGGAGTGTCATCCTGGGTTACTGCATAGGGACTTCCTCCGTCATCTGCATCC 1783

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702

Db       1784 CCACATACATTACCTACCGGCTGGTCACCACCCCAGGGACCCTGAAGGAGCGCATTATTA 1843

Qy       1703 CAATCCAACGTCCGGAA 1719

Db       1844 AAAGTATCACTCCAGAA 1860
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RESULT 5
RNSLC6A4
LOCUS       RNSLC6A4                2015 bp    mRNA    linear   ROD 12-AUG-1998
DEFINITION  R.norvegicus mRNA for serotonin transporter.
ACCESSION   Y11024
VERSION     Y11024.1  GI:1841937
KEYWORDS    serotonin receptor; SLC6A4 gene.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2015)
  AUTHORS   Smith,A.P.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-1997) A.P.L. Smith, Section of Respiratory
            Medicine, Sheffield University, Floor F, Medical School, Beech Hill
            Road, Sheffield S10 2RX, UK
REFERENCE   2  (bases 1 to 2015)
  AUTHORS   Gonzalez,A.M., Smith,A.P., Emery,C.J. and Higenbottam,T.W.
  TITLE     The pulmonary hypertensive fawn-hooded rat has a normal serotonin
            transporter coding sequence
  JOURNAL   Am. J. Respir. Cell Mol. Biol. 19 (2), 245-249 (1998)
  MEDLINE   98365414
   PUBMED   9698596
REFERENCE   3  (bases 1 to 2015)
  AUTHORS   Hoffman,B.J., Mezey,E. and Brownstein,M.J.
  TITLE     Cloning of a serotonin transporter affected by antidepressants
  JOURNAL   Science 254 (5031), 579-580 (1991)
  MEDLINE   92054541
   PUBMED   1948036
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  Matches  983;  Conservative    0;  Mismatches  651;  Indels    3;  Gaps    1;

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Db         449 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 508

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DEFINITION  Sequence 6 from Patent US 5418162.
ACCESSION   I12034
VERSION     I12034.1  GI:909475
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SOURCE      Unknown.
ORGANISM    Unknown.
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REFERENCE   1  (bases 1 to 2278)
  AUTHORS   Blakely,R.D., Caron,M.G. and Fremeau,R.T. Jr.
  TITLE     Serotonin transporter CDNA
  JOURNAL   Patent: US 5418162-A 6 23-MAY-1995;
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  Matches  983;  Conservative    0;  Mismatches  651;  Indels    3;  Gaps    1;

Qy         86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145

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REFERENCE   1  (bases 1 to 2415)
  AUTHORS   Blakely,R.D., Caron,M.G. and Fremeau,R.T. Jr.
  TITLE     Serotonin transporter CDNA
  JOURNAL   Patent: US 5418162-A 8 23-MAY-1995;
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  Best Local Similarity  60.0%;  Pred. No. 1.8e-123;
  Matches  983;  Conservative    0;  Mismatches  651;  Indels    3;  Gaps    1;

Qy          86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
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Qy        1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
               |||  |      |    |||||  | |      ||  ||||||   |  ||  |  ||||||  ||
Db        1284 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1343

Qy        1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
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Db        1344 ATGCAGAGGCAATAGCCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1403

Qy        1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
               ||  |  ||  ||  ||||||  |  |||||  ||  ||  |  |||  ||  ||  |  ||  |  |||  |||
Db        1404 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1463

Qy        1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
               |    ||  ||  |  ||||    |  |  |  ||    |  |||    ||  |||    |  ||
Db        1464 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1523

Qy        1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
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Db        1524 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1583

Qy        1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
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Db        1584 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1643

Qy        1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
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Db        1644 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1703

Qy        1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
               |   ||  |||  ||||||||  |||||||  |||  |||      ||||||  ||  |  ||  |  |
Db        1704 GCTTCAGCCCGGGATGGTTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1763

Qy        1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
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Db        1764 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1823

Qy        1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
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Db        1824 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1883

Qy        1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
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Db        1884 CTACCTATATCATTTATCGGCTGATCAGCACTCCGGGGACACTTAAGGAGCGCATTATTA 1943

Qy        1703 CAATCCAACGTCCGGAA 1719
                 ||       |||  |||
Db        1944 AAAGTATCACTCCTGAA 1960


RESULT 8
RRSERTRAN
LOCUS       RRSERTRAN              2415 bp    mRNA    linear   ROD 27-JUL-1992
DEFINITION  R.rattus mRNA for serotonin transporter.
ACCESSION   X63253
VERSION     X63253.1  GI:57742
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KEYWORDS    serotonin transporter.
SOURCE      Rattus rattus.
  ORGANISM  Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2278)
  AUTHORS   Blakely,R.D., Berson,H.E., Fremeau,R.T. Jr., Caron,M.G., Peek,M.M.,
            Prince,H.K. and Bradley,C.C.
  TITLE     Cloning and expression of a functional serotonin transporter from
            rat brain
  JOURNAL   Nature 354 (6348), 66-70 (1991)
  MEDLINE   92049754
   PUBMED   1944572
REFERENCE   2  (bases 1 to 2278)
  AUTHORS   Blakely,R.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1992) Randy D Blakely, Anatomy and Cell Biology,
            Emory University School, of Medicine, Atlanta, Georgia, 30322, USA
  REMARK    revised by [3]
  REFERENCE 3  (bases 1 to 2415)
  AUTHORS   Blakely,R.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-1992) Randy D Blakely, Anatomy and Cell Biology,
            Emory University School, of Medicine, Atlanta, Georgia, 30322, USA
FEATURES             Location/Qualifiers
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                     FSLGPGFGVLLAFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIFTVLGYMAEMRNE
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BASE COUNT      538 a    700 c    605 g    572 t
ORIGIN

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Qy        146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
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Qy        206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
Db        444 ACCAGAATGGCGGAGGGGCCTTCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGA 503

Qy        266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
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Qy        326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385
Db        564 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 623

Qy        386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
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Qy        446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505
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Qy        506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
Db        744 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 803

Qy        566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625
Db        804 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 863

Qy        626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
Db        864 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 923

Qy        686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
Db        924 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 983

Qy        746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
Db        984 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 1043

Qy        806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
Db       1044 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 1103

Qy        866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
Db       1104 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1163

Qy        926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
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Qy       1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
Db       1284 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1343

Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
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Qy       1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
Db       1404 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1463

Qy       1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
Db       1464 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1523

Qy       1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
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Db       1824 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1883

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702

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Qy       1703 CAATCCAACGTCCGGAA 1719

Db       1944 AAAGTATCACTCCTGAA 1960
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LOCUS       RNNTT                   3190 bp    mRNA    linear   ROD 29-JUL-1992
DEFINITION  R.norvegicus NTT mRNA.
ACCESSION   X63995
VERSION     X63995.1  GI:56779
KEYWORDS    neurotransmitter; neurotransmitter transporter; NTT gene.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3190)
  AUTHORS   Mayser,W., Betz,H. and Schloss,P.
  TITLE     Isolation of cDNAs encoding a novel member of the neurotransmitter
            transporter gene family
  JOURNAL   FEBS Lett. 295 (1-3), 203-206 (1991)
  MEDLINE   92111740
   PUBMED   1765155
REFERENCE   2  (bases 1 to 3190)
  AUTHORS   Mayser,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-1992) W. Mayser, MPI fuer Hirnforschung,
            Deutschordenstr 46, 6000 Frankfurt 71, FRG
COMMENT     See also M79450 & X63253.
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Qy         266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325

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Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162

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Qy       1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342

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Qy       1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402

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Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642

Db       1869 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1928

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702

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Qy       1703 CAATCCAACGTCCGGAA 1719

Db       1989 AAAGTATCACTCCTGAA 2005
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RESULT 10
AF013604
LOCUS       AF013604               2576 bp    mRNA    linear   ROD 11-JAN-2000
DEFINITION  Mus musculus serotonin transporter mRNA, complete cds.
ACCESSION   AF013604
VERSION     AF013604.1  GI:2338559
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2576)
  AUTHORS   Chang,A.S., Chang,S.M., Starnes,D.M., Schroeter,S., Bauman,A.L. and
            Blakely,R.D.
  TITLE     Cloning and expression of the mouse serotonin transporter
  JOURNAL   Brain Res. Mol. Brain Res. 43 (1-2), 185-192 (1996)
  MEDLINE   97189261
    PUBMED  9037532
REFERENCE   2  (bases 1 to 2576)
  AUTHORS   Chang,A.S. and Chang,S.M.
  TITLE     Nongenomic steroidal modulation of high-affinity serotonin
            transport
  JOURNAL   Biochim. Biophys. Acta 1417 (1), 157-166 (1999)
  MEDLINE   99177451
    PUBMED  10076044
REFERENCE   3  (bases 1 to 2576)
  AUTHORS   Chang,A.S., Chang,S.M., Starnes,D.M., Schroeter,S., Bauman,A.L. and
            Blakely,R.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1997) Rammelkamp Center for Research, MetroHealth
            Medical Center, 2500 MetroHealth Drive, Cleveland, OH 44109, USA
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BASE COUNT      604 a    684 c    621 g    667 t
ORIGIN
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  Query Match             32.8%;  Score 578.2;  DB 10;  Length 2576;
  Best Local Similarity   59.7%;  Pred. No. 3.3e-123;
  Matches  988;  Conservative    0;  Mismatches  663;  Indels    3;  Gaps    1;

Qy         86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145

Db        210 TGGTGGCTGAGATTCACCAAGGGGAACGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC 269

Qy        146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205

Db        270 TGTCTGTCATTGGCTATGCCGTGGACCTGGGCAACATCTGGCGTTTTCCCTACATATGCT 329

Qy        206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265

Db        330 ACCAGAATGGTGGAGGGGCCTTCCTCCTCCCTTACACCATCATGGCCATCTTTGGGGGGA 389

Qy        266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325

Db        390 TCCCGCTCTTCTACATGGAGCTCGCCCTGGGCCAGTACCACCGAAATGGGTGCATTTCTA 449

Qy        326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385

Db        450 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGCTATGCCATCTGCATCATTGCCT 509

Qy        386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445

Db        510 TTTATATCGCCTCCTACTATAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 569

Qy        446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505

Db        570 CCTTCACGGACCAGCTGCCCTGGACCAGCTGCAAGAACTCTTGGAACACTGGCAACTGCA 629

Qy        506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
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Db        630 CCAACTACTTCGCCCAGGACAACATCACCTGGACACTCCATTCCACGTCACCTGCTGAGG 689

Qy        566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625

Db        690 AGTTTTACTTGCGCCATGTCCTGCAGATCCATCAGTCAAAGGGACTCCAGGACCTGGGGA 749

Qy        626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685

Db        750 CCATCAGCTGGCAGCTGGCTCTCTGCATCATGCTCATCTTCACCATTATCTACTTCAGCA 809

Qy        686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745

Db        810 TCTGGAAAGGAGTCAAAACGTCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTACA 869

Qy        746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805

Db        870 TTGTCCTTTCTGTCCTGCTGGTGAGGGGAGCCACCCTTCCTGGAGCCTGGAGAGGGGTTG 929

Qy        806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865

Db        930 TCTTTTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTTGATGCTG 989

Qy        866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925

Db        990 CGGCTCAGATCTTTTTCTCTCTTGGCCCGGGGTTTGGGGTTCTCCTGGCGTTTGCTAGCT 1049

Qy        926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985

Db       1050 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1109

Qy        986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045

Db       1110 TGACGAGCTTCGTCTCTGGCTTTGTCATCTTCACGGTGCTTGGCTACATGGCTGAGATGA 1169

Qy       1046 AGAACAAGAGCAT---CGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102

Db       1170 GGAACGAAGACGTGTCCGAGGTGGCCAAAGACGCGGGCCCCAGCCTCCTTTTCATCACAT 1229

Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162

Db       1230 ATGCGGAGGCAATAGCTAACATGCCAGCATCCACATTCTTTGCCATCATCTTCTTCCTCA 1289

Qy       1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222

Db       1290 TGTTAATCACGCTGGGTTTGGATAGCACGTTTGCAGGCCTGGAAGGTGTGATCACAGCTG 1349

Qy       1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282

         1350 TGTTGGATGAGTTTCCTCACATCTGGGCCAAGCGCAGGGAATGGTTTGTGCTCATCGTGG 1409

         1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342

Db       1410 TCATCACTTGCATCTTGGGATCCCTGCTCACACTGACATCAGGAGGGGCGTATGTGGTGA 1469

Qy       1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402

Db       1470 CCCTGCTGGAGGAGTACGCCACGGGGCCAGCAGTGCTCACTGTGGCTCTCATCGAGGCCG 1529

Qy       1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462

Db       1530 TCGTCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGACGTGAAGGAAATGCTGG 1589

Qy       1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522

Db       1590 GCTTCAGCCCCGGATGGTTTTGGAGGATCTGCTGGGTGGCCATCAGTCCTCTGTTTCTCC 1649

Qy       1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582

Db       1650 TGTTCATCATTTGCAGTTTTTTGATGAGTCCACCCCAACTCCGGCTTTTCCAATACAATT 1709

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642

Db       1710 ATCCCCACTGGAGTATCATCTTGGGCTACTGCATAGGAACATCGTCTGTCATCTGCATCC 1769

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702

Db       1770 CTATATACATCATTTATCGGCTGATCAGCACTCCAGGGACACTTAAGGAGCGCATTATTA 1829

Qy       1703 CAATCCAACGTCCGGAAGTGACGTCGATACCTCC 1736

Db       1830 AAAGTATCACTCCTGAAACACCAACGGAAATTCC 1863
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RESULT 11
AF119122

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LOCUS       AF119122               2595 bp    mRNA    linear   MAM 21-JUL-1999
DEFINITION  Bos taurus serotonin transporter mRNA, complete cds.
ACCESSION   AF119122
VERSION     AF119122.1  GI:4588917
KEYWORDS    .
SOURCE      Bos taurus.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 2595)
  AUTHORS   Mortensen,O.V., Kristensen,A.S., Rudnick,G. and Wiborg,O.
  TITLE     Molecular cloning, expression and characterization of a bovine
            serotonin transporter
  JOURNAL   Brain Res. Mol. Brain Res. 71 (1), 120-126 (1999)
  MEDLINE   99337805
   PUBMED   10407194
REFERENCE   2  (bases 1 to 2595)
  AUTHORS   Mortensen,O.V. and Wiborg,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JAN-1999) Psychiatric University Hospital, Lab of
            Molecular Neurobiology, Skovagervej 2, Risskov 8240, Denmark
FEATURES             Location/Qualifiers
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                     TWTLHSTSPAEEFYTRHVLQIHRSKGLQDLGGLSWQLVLCIMFIFTVIYFSIWKGVKT
                     SGKVVWVTATFPYIILLILLVRGATLPGAWRGVLFYLKPNWQKLLETGVWVDAAAQIF
                     FSLGPGFGVLLAFASYNKFHNNCYQDALVTSAVNCMTSFVSGFVIFTVLGYMAEMRKE
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                     AVAVFWFYGINQFCSDVKEMLGFSPGWFWKICWVAISPLFLLFIICSFLMSPPQLRLF
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     polyA_signal    2462. .2466
     polyA_site      2581
BASE COUNT      611 a    670 c    625 g    689 t
ORIGIN
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  Query Match             32.0%;  Score 563.8;  DB 4;  Length 2595;
  Best Local Similarity   59.4%;  Pred. No. 7.2e-120;
  Matches  969;  Conservative    0;  Mismatches  658;  Indels    3;  Gaps    1;

Qy        110 AGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAGTGG 169

Db        252 AGCGGGAGACCTGGGCCAAGAAGGTGGATTTCCTCCTCTCTGTCATTGGCTATGCTGTGG 311

Qy        170 ATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGTTCC 229

Db        312 ACCTGGGCAACGTCTGGCGCTTTCCCTACATTTGTTACCAGAATGGAGGGGGGGCGTTCC 371
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Qy       230 TGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAACTGG 289
Db       372 TCCTTCCCTACACTATCATGGCCATTTTTGGGGGGATCCCGCTCTTCTACATGGAGCTCG 431

Qy       290 CGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCGCGC 349
Db       432 CACTGGGGCAGTACCACCGAAATGGATGCATTTCGATATGGACAAAAATCTGCCCAATTT 491

Qy       350 TTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACAACA 409
Db       492 TCAAAGGGATAGGTTGCGCCATCTGCCTCATCGCCTTCTACATCGCCTCCTACTACAACA 551

Qy       410 CGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTGTGC 469
Db       552 CCATCATAGCCTGGGCCCTCTACTACCTCATCTCCTCCTTCACGGAGCAGCTGCCCTGGA 611

Qy       470 TGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCTCAC 529
Db       612 CCAGCTGCGAGAACTCCTGGAACACTGGCAACTGCACCAACTACTTCTCCGAGGATAACA 671

Qy       530 CTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTATTGG 589
Db       672 TCACCTGGACGCTCCACTCAACGTCCCCTGCAGAAGAATTTTACACGCGGCACGTCCTGC 731

Qy       590 AGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTCTGT 649
Db       732 AGATCCACCGGTCGAAGGGGCTCCAGGACCTGGGGGGCCTCAGTTGGCAGCTTGTCCTGT 791

Qy       650 GTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTGCTG 709
Db       792 GCATCATGTTCATCTTCACTGTTATCTACTTTAGCATCTGGAAAGGCGTCAAAACATCTG 851

Qy       710 GCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGGCGA 769
Db       852 GCAAGGTGGTTTGGGTGACAGCCACCTTCCCTTACATCATTCTTTTGATCCTGCTGGTGA 911

Qy       770 GAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGTGGC 829
Db       912 GGGGGGCCACCCTCCCTGGAGCCTGGAGGGGAGTTCTCTTCTATTTGAAACCCAACTGGC 971

Qy       830 ACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGCTCG 889
Db       972 AGAAACTCCTAGAGACGGGGGTGTGGGTGGATGCAGCCGCCCAGATCTTCTTCTCTCTCG 1031

Qy       890 GTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACTGCT 949
Db      1032 GCCCTGGCTTTGGGGTCCTACTGGCTTTTGCGAGCTACAACAAATTCCACAACAACTGTT 1091

        950 ACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTTTCG 1009
Db      1092 ACCAAGACGCCCTGGTGACCAGTGCAGTGAATTGCATGACGAGCTTCGTTTCAGGATTTG 1151

Qy      1010 TCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGGTTG 1069
Db      1152 TCATCTTCACAGTGCTGGGGTATATGGCTGAGATGAGGAAAGAAGATGTGTCTGAGGTGG 1211

Qy      1070 GCCTCGA---AGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCATGA 1126
Db      1212 CCAAAGATGCAGGCCCCAGCCTCCTGTTCATCACATACGCAGAAGCCATAGCCAACATGC 1271

Qy      1127 CCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTGACA 1186
Db      1272 CAGCATCCACATTCTTTGCCATCGTCTTCTTCCTGATGTTAATCACCCTGGGCTTGGACA 1331

Qy      1187 GTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAGTGT 1246
Db      1332 GCACGTTTGCAGGCTTGGAGGGGGTGATCACAGCTGTGCTAGATGAGTTTCCACATGTCT 1391

Qy      1247 TAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCGCTC 1306
Db      1392 GGGCCAAGCGCCGGGAGTGGTTTGTGCTTGGCGTGGTCATTACCTGCTTCTTTGGATCTC 1451

Qy      1307 TGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCCCTG 1366
Db      1452 TGGTCACCTTGACTTTCGGCGGGGCCTATGTGGTGAAGCTGTTGGAGGAGTTCGCCACGG 1511

Qy      1367 GATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATGGCG 1426
Db      1512 GACCTGCAGTGCTCACCGTGGCCCTGATTGAAGCAGTTGCTGTGTTTTGGTTCTACGGCA 1571

Qy      1427 TCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCTGGA 1486
Db      1572 TCAATCAGTTCTGCAGTGATGTGAAGGAAATGCTTGGTTTCAGCCCTGGATGGTTCTGGA 1631

Qy      1487 GGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCGTTC 1546
Db      1632 AGATCTGCTGGGTAGCCATCAGTCCTCTGTTTCTCCTGTTCATCATCTGCAGTTTTTTGA 1691

Qy      1547 TGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCGTAG 1606
Db      1692 TGAGCCCACCACAGCTACGACTTTTCCAGTATGATTATCCTCGGTGGAGCATCATCCTGG 1751

Qy      1607 GCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAACTGC 1666
Db      1752 GTTACTGCATAGGAACCTCATCTTTCATCTGCATCCCCACATATATAACCTATCGGCTGA 1811

Qy      1667 TCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAATCCAACGTCCGGAAGTGACGT 1726
Db      1812 TTGTCACTCCAGGGACACTTAAGGAGCGTATTATTAAAGGTATCACGCCAGAAACACCGA 1871

Qy      1727 CGATACCTCC 1736
Db      1872 CAGCAATTCC 1881
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RESULT 12
MMSEROT
LOCUS       MMSEROT                 2357 bp    mRNA    linear   ROD 25-SEP-1996
DEFINITION  M.musculus mRNA for serotonin transporter, partial.
ACCESSION   X66119
VERSION     X66119.1  GI:312495
KEYWORDS    glutamate receptor; glutamate receptor subunit.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2357)
  AUTHORS   Gregor,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-1992) P. Gregor, National Inst on Drug Abuse,
            Molecular Neurobiology Lab, Box 5180, Baltimore MD 21224, USA
REFERENCE   2  (bases 1 to 2357)
  AUTHORS   Gregor,P., Patel,A., Shimada,S., Lin,C.L., Rochelle,J.,
            Kitayama,S., Seldin,M. and Uhl,G.R.
  TITLE     Murine serotonin transporter: sequence and localization to
            Chromosome II
  JOURNAL   Mamm. Genome 3, 283-284 (1993)
FEATURES             Location/Qualifiers
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                     /strain="balb/c"
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ORIGIN

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  Best Local Similarity   60.2%;  Pred. No. 1.2e-119;
  Matches  995;  Conservative    0;  Mismatches  642;  Indels   17;  Gaps    3;
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Qy        86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
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Db         5 TGGTGGCTGAGATTCACCAAGGGGAACGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC  64

Qy       146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
             || | ||  | || |  || ||||| || || ||| | |||| || ||||||| || |
Db        65 TGTCTGTCATTGGCTATGCCGTGGACCTGGGCAACATCTGGCGTTTTCCCTACATATGCT 124

Qy       206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
             |||||||||| || || || |||||  |||| |||  | | |||    | |||||  |||
Db       125 ACCAGAATGGTGGAGGGGCCTTCCTCCTCCCTTACACCATCATGGCCATCTTTGGGGGGA 184

Qy       266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
             | ||||| |||| | |||| || || |||||||||||||||||    || ||| |  ||
Db       185 TCCCGCTCTTCTACATGGAGCTCGCCCTGGGCCAGTACCACCGAAATGGGTGCATTTCTA 244

Qy       326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385
             | ||||    ||||||||||      | |||||  | |||||||||||||||||| || | |
Db       245 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGCTATGCCATCTGCATCATTGCCT 304

Qy       386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
             | || || | |   ||||| ||||| ||||| |  |||||| | || |||||  ||| | |
Db       305 TTTATATCGCCTCCTACTATAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 364

Qy       446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505
             |  || ||   |  | ||     | |||| ||  || ||   |      ||
Db       365 CCTTCACG--GACCAGCTGCAAGAACTCTTGGAACACTGGCAACTGCACCAACTACTTCG 422

Qy       506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
             | | |  ||       |    ||| ||  | |            | |||| ||  |||
Db       423 CCCAGGACAACATCACCTGGACACTCCATTCCA-----------CGTCACCTGCTGAGG 470

Qy       566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625
             |||| | |   ||  |||| || ||   ||  |||| || || ||  | ||| |||||
Db       471 AGTTTTACTTGCGCCATGTCCTGCAGATCCATCAGTCAAAGGGACTCCAGGACCTGGGGA 530

Qy       626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
             | ||||    |  |||||||||| ||  |  |     ||||   | |  |||||||| |
Db       531 CCATCAGCTGGCAGCTGGCTCTCTGCATCATGCTCATCTTCACCATTATCTACTTCAGCA 590

Qy       686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
             | |||||||||||||  |  |||||||||||||||||||||||||      ||| |||
Db       591 TCTGGAAAGGAGTCAAAACGTCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTACA 650

Qy       746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
             . | ||  |  |||||| ||| || | ||| ||||| ||||    |   ||  |
Db       651 TTGTCCTTTCTGTCCTGCTGGTGAGGGGAGCCACCCTTCCTGGAGCCTGGAGAGGGGTTG 710

             806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
              ||  ||| | |  ||  | ||||| ||| |     |  |   ||| ||| |||| || |
             711 TCTTTTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTTGATGCTG 770

Qy       866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
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Db       771 CGGCTCAGATCTTTTTCTCTCTTGGCCCGGGGTTTGGGGTTCTCCTGGCGTTTGCTAGCT 830

Qy       926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
             |||||||||||||||||||||| |||   || || ||  | ||   |   | ||||||
Db       831 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 890

Qy       986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045
             |||| ||||||  |  |||| || ||||| ||| |||   | || ||||||||   |  |
Db       891 TGACGAGCTTCGTCTCTGGCTTTGTCATCTTCACGGTGCTTGGCTACATGGCTGAGATGA 950

Qy      1046 AGAACAAGAGCAT---CGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
              |||| |   | |  |||||  ||       ||  |||||  | ||  | ||||||   |
Db       951 GGAACGAAGACGTGTCCGAGGTGGCCAAAGACGCGGGCCCCAGCCTCCTTTTCATCACAT 1010

Qy      1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
             |  | |||||  || || | |||| | |  |||   ||||  ||||||||||||||||||
Db      1011 ATGCGGAGGCAATAGCTAACATGCCAGCATCCACATTCTTTGCCATCATCTTCTTCCTCA 1070

Qy      1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
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Db      1071 TGTTAATCACGCTGGGTTTGGATAGCACGTTTGCAGGCCTGGAAGGTGTGATCACAGCTG 1130

Qy      1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
             | |  || || | |||||   | |  | ||  |   | |||   ||||||    |  ||
Db      1131 TGTTGGATGAGTTTCCTCACATCTGGGCCAAGCGCAGGGAATGGTTTGTGCTCATCGTGG 1190

Qy      1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
             |  |       |    |  |  | |||| |||    ||||  || || |  ||  | ||
Db      1191 TCATCACTTGCATCTTGGGATCCCTGCTCACACTGACATCAGGAGGGGCGTATGTGGTGA 1250

Qy      1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
              ||| ||  | | ||| | | | ||    ||  | ||    ||||   |    |||||
Db      1251 CCCTGCTGGAGGAGTACGCCACGGGGCCAGCAGTGCTCACTGTGGCTCTCATCGAGGCCG 1310

Qy      1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
              || |||||  ||| | |||||  ||   | |||||     || |||| |   |||||||
Db      1311 TCGTCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGACGTGAAGGAAATGCTGG 1370

Qy      1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
             |   || ||| |||||||| ||||||| ||| |||     |||||||||  | ||  | |
Db      1371 GCTTCAGCCCCGGATGGTTTTGGAGGATCTGCTGGGTGGCCATCAGTCCTCTGTTTCTCC 1430

Qy      1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
             || |  |  |       |  |  ||   |      |  | |           ||||||  |
Db      1431 TGTTCATCATTTGCAGTTTTTTGATGAGTCCACCCCAACTCCGGCTTTTCCAATACAATT 1490

Qy      1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
             |||||   |||  |||||  | | ||||     ||        |  | |||   |||||  |
Db      1491 ATCCCCACTGGAGTATCATCTTGGGCTACTGCATAGGAACATCGTCTGTCATCTGCATCC 1550

Qy      1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
             || | ||||| || ||    ||| ||| |||||| || |     |   | ||||| |  |
Db      1551 CTATATACATCATTTATCGGCTGATCAGCACTCCAGGGACACTTAAGGAGCGCATTATTA 1610

Qy      1703 CAATCCAACGTCCGGAAGTGACGTCGATACCTCC 1736
              ||      ||| |||    |  ||  |  |||
Db      1611 AAAGTATCACTCCTGAAACACCAACGGAAATTCC 1644
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RESULT 13
AF285761
LOCUS       AF285761               2207 bp    mRNA    linear   PRI 14-MAR-2001
DEFINITION  Macaca mulatta serotonin transporter mRNA, complete cds.
ACCESSION   AF285761
VERSION     AF285761.1  GI:9664874
KEYWORDS    .
SOURCE      Macaca mulatta.
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 2207)
  AUTHORS   Miller,G.M., Yatin,S.M., De La Garza,R. II, Goulet,M. and
            Madras,B.K.
  TITLE     Cloning of dopamine, norepinephrine and serotonin transporters from
            monkey brain: relevance to cocaine sensitivity
  JOURNAL   Brain Res. Mol. Brain Res. 87 (1), 124-143 (2001)
  MEDLINE   21126513
   PUBMED   11223167
REFERENCE   2  (bases 1 to 2207)
  AUTHORS   Miller,G.M. and Madras,B.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-2000) Neurochemistry, New England Regional
            Primate Research Center, Harvard Medical School, One Pine Hill
            Drive, Southborough, MA 01772, USA
FEATURES             Location/Qualifiers
     source          1. .2207
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                     /db_xref="taxon:9544"
                     /tissue_type="midbrain raphe"
     CDS             1. .1893
                     /codon_start=1
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                     /product="serotonin transporter"
                     /protein_id="AAF97247.1"
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                     NGYSAVPSPGAGDDTRHSIPAATTTLVAELHQGERETWGKKVDFLLSVIGYAVDLGNV
                     WRFPYICYQNGGGAFLIPYTIMAIFGGIPLFYMELALGQYHRNGCISIWRKICPIFKG
                     IGYAICIIAFYIASYYNTIMAWALYYLISSFTDQLPWTSCKNSWNTGNCTNYFSEDNI
                     TWTLHSTSPAEEFYTRHVLQIHRSKGLQDLGGISWQLALCIMLIFTVIYFSIWKGVKT
                     SGKVVWVTATFPYIILSVLLVRGATLPGAWRGVLFYLKPNWQKLLETGVWIDAAAQIF
                     FSLGPGFGVLLAFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIFTVLGYMAEMRNE
                     DVSEVAKDAGPSLLFITYAEAIANMPASTFFAIIFFLMLITLGLDSTFAGLEGVITAV
                     LDEFPHIWAKRREWFVLAVVITCFFGSLVTLTFGGAYVVKLLEEYATGPAVLTVALIE
                     AVAVSWFYGITQFCRDVKEMLGFSPGWFWRICWVAISPLFLLFIICSFLMSPPQLRLF
                     QYNYPHWSIILGYCIGTSSFVCIPTYIAYRLISTPGTFKERIIKSITPETPTEIPCGD
                     VRLNAV"
BASE COUNT      486 a    607 c    567 g    547 t
ORIGIN

  Query Match           31.9%;  Score 562;  DB 9;  Length 2207;
  Best Local Similarity 59.9%;  Pred. No. 1.9e-119;
  Matches  959;  Conservative    0;  Mismatches  640;  Indels    3;  Gaps    1;

Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
Db        230 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTCCTCTCAGTCATTGGCTATGCTG 289

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
Db        290 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGAGGGGCAT 349

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
Db        350 TCCTCATCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 409

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
Db        410 TCGCGCTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 469

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
Db        470 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCCTCCTACTACA 529

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
Db        530 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 589

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
Db        590 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCTGAGGACA 649

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
Db        650 ACATCACCTGGACCCTCCATTCCACCTCCCCAGCTGAAGAATTTTACACGCGCCACGTCC 709

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
Db        710 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 769

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
Db        770 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 829

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
Db        830 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 889

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
Db        890 TGAGGGGCGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAACT 949

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
Db        950 GGCAGAAACTCCTAGAGACAGGGGTGTGGATAGATGCAGCTGCTCAGATCTTCTTCTCTC 1009

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
Db       1010 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1069

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
Db       1070 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1129

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
Db       1130 TTGTCATCTTCACGGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1189

Qy       1067 TTGGCCTCGA---AGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
Db       1190 TGGCCAAAGATGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1249

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
Db       1250 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1309

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
Db       1310 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACAGCTGTGCTGGATGAGTTCCCACACA 1369

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
Db       1370 TCTGGGCCAAGCGCCGGGAGTGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1429

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
Db       1430 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTACGCCA 1489

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
Db       1490 CGGGGCCTGCAGTGCTCACTGTCGCGCTGATCGAGGCAGTCGCTGTGTCTTGGTTCTATG 1549

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
Db       1550 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTGGGCTTCAGCCCGGGCTGGTTCT 1609

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
Db       1610 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1669

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
Db       1670 TGATGAGCCCACCACAGCTACGACTTTTCCAATATAATTATCCCCACTGGAGTATCATCT 1729

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
Db       1730 TGGGTTACTGCATAGGAACCTCATCTTTCGTCTGCATCCCCACATACATAGCTTATCGGC 1789

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
Db       1790 TGATCAGCACTCCAGGGACATTTAAGGAGCGTATTATTAAAA 1831


RESULT 14
RATSTRP
LOCUS       RATSTRP                 2751 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Rat serotonin transporter mRNA, complete cds.
ACCESSION   M79450
VERSION     M79450.1  GI:207086
KEYWORDS    serotonin transporter.
SOURCE      Rattus norvegicus cDNA to mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2751)
  AUTHORS   Hoffman,B.J., Mezey,E. and Brownstein,M.J.
  TITLE     Cloning of a serotonin transporter affected by antidepressants
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  JOURNAL   Science 254 (5031), 579-580 (1991)
  MEDLINE   92054541
   PUBMED   1948036
FEATURES             Location/Qualifiers
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                     /cell_type="Basophilic leukemia cell"
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                     /gene="5HT"
     mRNA            1. .2751
                     /partial
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                     membrane"
     CDS             232. .2193
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                     /protein_id="AAA42186.1"
                     /db_xref="GI:207087"
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                     FSLGPGFGVLLAFASYNKFNNNCYQDALVTSVVNCMTSFVSGFVIFTVLGYMAEMRNE
                     DVSEVAKDAGPSLLFITYAEAIGNMPASTFFAIIFFLMLITLGLDSTFAGLEGVITAV
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                     AVAVSWFYGITQFCSDVKEMLGFSGMVWRICWVAISPLFLLFIICSFLMSPPQLRLFQ
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BASE COUNT      619 a    782 c    689 g    661 t
ORIGIN

  Query Match             31.5%;  Score 555.4;  DB 10;  Length 2751;
  Best Local Similarity   59.6%;  Pred. No. 6.4e-118;
  Matches  975;  Conservative    0;  Mismatches  656;  Indels    6;  Gaps    2;

          86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
             ||||| |    |  |       || |||| ||||||||||  ||||||   || ||||| |
         440 TGGTGGCTGAGATTCGCCAAGGGGAGCGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC 499

Qy       146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
             || | ||  | || |  || ||||| || || ||| | ||||| || || ||||| || | 
Db       500 TGTCCGTCATTGGCTATGCCGTGGACCTGGGCAACATCTGGCGGTTTCCTTACATATGCT 559

Qy       206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
             |||||||||| || || || |||||  |||| ||   | | |||    | || || |||
Db       560 ACCAGAATGGCGGAGGGGCCTTCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGA 619

Qy       266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
             | ||||| || | | |||| || || ||||||||||||||||   ||| ||| |  |
Db       620 TCCCGCTCTTTTACATGGAGCTCGCACTGGGCCAGTACCACCGAAACGGGTGCATTTCCA 679

Qy       326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385
             | ||||    |||||||||      | |||||  | || || ||||||||||| |||| |
Db       680 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 739

Qy       386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
             | ||||| | |   |||||||||| ||||| |  |||||| | || ||||| ||| | |
Db       740 TTTACATCGCCTCCTACTACAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 799

Qy       446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505

                 | ||| ||          |   |       || || | || |   |||    | |||
Db       800 CCCTCACGGACCGGCTGCCCTGGACCAGCTGCACGAACTCCTGGAACACTGGCAACTGCA 859

Qy       506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
             |    | |    |          |             | |   | ||  |  | || ||  |||
Db       860 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 919

Qy       566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625
             |||||| |   ||  ||||  || ||   ||| ||||||| || ||  | ||| ||||
Db       920 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 979

Qy       626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
             | |||||    |  |||| |||| ||  |  |     ||||   | |  |||||||   |
Db       980 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 1039

Qy       686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
             | |||||||| ||||  |  |||||||||||||||||||||||||||      ||| |||
Db      1040 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 1099

Qy       746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
             | ||  ||     | ||||||| ||| || | ||| ||||| |||||    |    ||  |
Db      1100 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 1159

Qy       806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
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Db      1160 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 1219

Qy       866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
             | | ||||| |||||||| || || || || ||  ||  |||  | | ||||
Db      1220 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1279

Qy       926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
             |||||||||||||||||||||| |||   || || ||  | ||   |    | ||||||
Db      1280 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1339

Qy       986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045
             |||| |||||| |  |||| |||||||| ||| ||||  | || |||||||||  |  |
Db      1340 TGACAAGCTTCGTCTCTGGCTTCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGA 1399

Qy      1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
             |||  |     |    |||||| | |    || ||||||  | ||  | ||||||  ||
Db      1400 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1459

Qy      1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
             |  | ||||| || | || |||| | |  |||  |||||  ||||||||||||||||||
Db      1460 ATGCAGAGGCAATAGGCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1519

Qy      1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
             || | || || |||||| | ||||| || || | ||| || || |  || | ||| |||
Db      1520 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1579

Qy      1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
             |    || || | |||   | |  | || |   | |||   || ||| |   | ||
Db      1580 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1639

Qy      1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
             |  |       |   | |  | |||| |||    || |  || || | |||| | ||
Db      1640 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1699

Qy      1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
               || ||  | | ||||| | | ||    ||  | ||   |||||   |    |||||
Db      1700 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1759

Qy      1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
             || ||||  ||| | ||||| ||   | ||||      |||||| |   |||||||
Db      1760 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1819

Qy      1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
             |   || |   ||   | | ||||||| ||| |||      |||||| ||  | ||  | |
Db      1820 GCTTCAGC---GGGATGGTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1876

Qy      1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
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Db       1877 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1936

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
              |||||   |||  ||||  | | ||||      ||          |  |||||   ||||| |
Db       1937 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1996

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
              ||   || || || ||    ||| ||| |||||| || |      |   | || || |  |
Db       1997 CTACCTATATCATTTATCGGCTGATCAGCACTCCGGGGACACTTAAGGAGCGGATTATTA 2056

Qy       1703 CAATCCAACGTCCGGAA 1719
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Db       2057 AAAGTATCACTCCTGAA 2073


RESULT 15
I25791
LOCUS       I25791                2756 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5552308.
ACCESSION   I25791
VERSION     I25791.1  GI:1605661
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2756)
  AUTHORS   Hoffman,B.J., Mezey,E. and Brownstein,M.J.
  TITLE     CDNA clone of a rat serotonin transporter and protein encoded
            thereby
  JOURNAL   Patent: US 5552308-A 1 03-SEP-1996;
FEATURES             Location/Qualifiers
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BASE COUNT      624 a    782 c    689 g    661 t
ORIGIN

  Query Match           31.5%;  Score 555.4;  DB 6;  Length 2756;
  Best Local Similarity   59.6%;  Pred. No. 6.4e-118;
  Matches  975;  Conservative    0;  Mismatches  656;  Indels    6;  Gaps    2;

Qy         86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
              |||||  |    |  |       || |||| ||||||||||  ||||||   || ||||| |
Db        440 TGGTGGCTGAGATTCGCCAAGGGGAGCGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC 499

Qy        146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
              || | ||  | || |  || ||||| || || ||| | ||||| || || ||||| || | |
Db        500 TGTCCGTCATTGGCTATGCCGTGGACCTGGGCAACATCTGGCGGTTTCCTTACATATGCT 559

            206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
              |||||||||| || || || |||||  |||| ||   | | |||    | || || |||
Db        560 ACCAGAATGGCGGAGGGGCCTTCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGA 619

Qy        266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
              | ||||| || | | |||| || || ||||||||||||||||||   ||| ||| | | |
Db        620 TCCCGCTCTTTTACATGGAGCTCGCACTGGGCCAGTACCACCGAAACGGGTGCATTTCCA 679

Qy        326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385
              | ||||   |||||||||     | |||||  | || || ||||||||||| |||| |
Db        680 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 739

Qy        386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
              | ||||| | |   |||||||||||| ||||| |  |||||| | || |||||  ||| | |
Db        740 TTTACATCGCCTCCTACTACAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 799

Qy        446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505
              | ||| ||          |   |      || || | || |   |||    | |||
Db        800 CCCTCACGGACCGGCTGCCCTGGACCAGCTGCACGAACTCCTGGAACACTGGCAACTGCA 859

Qy        506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
              |   | |    |          |            | |  | ||  |  | || ||  |||
Db        860 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 919

Qy        566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625

              |||||| |   ||  ||||  || ||   ||| ||||||| || ||  | ||| ||||
Db        920 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 979

Qy        626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
              | ||||     | |||| |||| ||  |  |      ||||   | |  |||||||   |
Db        980 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 1039

Qy        686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
              | |||||||| |||| |  |||||||||||||||||||||||||       ||| |||
Db       1040 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 1099

Qy        746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
              | || ||    .| |||||||  ||| || | ||| |||||  |||||    |   ||  |
Db       1100 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 1159

Qy        806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
              || |||| | |  ||  | |||||  ||| |      |  |   ||| ||| | || || |
Db       1160 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 1219

Qy        866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
              |  | ||||| |||||||| || || || || || ||    || |||||  |  | ||||
Db       1220 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1279

Qy        926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
              |||||||||||||||||||| |||   || || ||  | ||   |   | ||||||
Db       1280 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1339

Qy        986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045
              |||| |||||| |  |||| |||||||| ||| ||||  | || |||||||||  |  |
Db       1340 TGACAAGCTTCGTCTCTGGCTTCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGA 1399

Qy       1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
              |||  |      |  ||||| | |    || ||||||  | ||  | ||||||  ||
Db       1400 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1459

Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
              |  | ||||| || | || |||| | |  ||| |||||  ||||||||||||||||||||
Db       1460 ATGCAGAGGCAATAGGCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1519

Qy       1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
              || | || || |||||| | ||||| || || | ||| || || |  || | ||| |||
Db       1520 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1579

Qy       1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
              |    || || |  |||   | |  | || |   | |||   || |||    |  ||
Db       1580 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1639

Qy       1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
              | |      |    | |  | |||| |||    || |  || || | |||| | ||
Db       1640 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1699

Qy       1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
              || ||  | | |||||  | | ||   ||  | ||  |||||   |   |||||  |
Db       1700 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1759

Qy       1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
              || |||||  ||| | |||||  ||   | |||||     |||||||  |  |||||||
Db       1760 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1819

Qy       1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
              |   || |  ||  | | |||||| ||| |||    ||||| ||  | || | |  | |
Db       1820 GCTTCAGC---GGGATGGTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1876

Qy       1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
              || |  |  |     |  | ||  |     || | |              |||||| ||
Db       1877 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1936

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
              |||||   |||  ||||  | | ||||      ||          |  |||||   ||||| |
Db       1937 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1996

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
              ||   || || || ||    ||| ||| |||||| || |      |   | || || |  |
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Db       1997 CTACCTATATCATTTATCGGCTGATCAGCACTCCGGGGACACTTAAGGAGCGGATTATTA 2056

Qy       1703 CAATCCAACGTCCGGAA 1719
                ||       ||| |||
Db       2057 AAAGTATCACTCCTGAA 2073
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Search completed: July 18, 2003, 15:18:42
Job time : 3126 secs